

REMARKS

In the Official Action dated May 23, 2003, claims 22-40 have been rejected under 35 U.S.C. §112, second paragraph as allegedly indefinite. Claims 22-40 have also been rejected under 35 U.S.C. §112, first paragraph as allegedly lacking enabling support. Claims 22-40 have also been rejected under 35 U.S.C. §101 and 35 U.S.C. §112, first paragraph as allegedly lacking a credible asserted utility or a well-established utility. The pending claims are free of the prior art.

This response addresses each of the Examiner's rejections. Favorable consideration of all pending claims is therefore respectfully requested.

Claims 22-40 has been rejected under 35 U.S.C. §112, second paragraph as allegedly indefinite. The Examiner contends that "normalizing total surface exposure" is unclear because there is no antecedence in the preceding step. In response, Applicants submit that the normalization step refers to backbone protein configurations that are comprised of amino acid sequences. As noted in the specification, at page 7, lines 4-15, non-self-intersecting configurations of dihedral angle pairs of amino acids are calculated whereby the surface exposure of each amino acid in the given configuration is divided by the total surface exposure of that configuration. "Total surface" exposure refers to the surface accessible to a sphere with a radius typical of a water molecule, see e.g. page 8, lines 25-31, for example.

The Examiner objects to the term "random set of sequences" in regard to hydrophobicities. Applicants submit that the random set refers to amino acid sequences. Applicants respectfully direct the Examiner's attention to page 9, lines 27-31 wherein hydrophobicities of amino acids are assigned a value and a set of sequences of hydrophobicities of uniform weight is randomly generated. The generation of a random set of values is a well-

known technique fully appreciated by the skilled artisan that requires no undue experimentation. A “uniform weight” is similarly well known to the skilled artisan in the context of generation of amino acid sequences and refers to the spacing between amino acids (see e.g., page 9, lines 23-31). Applicants further submit that the “determining” step functions to determine for each randomly generated sequence, which of the remaining configurations comprises a ground state. The “synthesizing” step has also been objected to. Applicants respectfully direct the Examiner’s attention to the specification at page 12, lines 29-30, wherein any art recognized method of protein synthesis may be employed.

Claim 27 has been objected to as allegedly claiming a step that is duplicative of a step in claim 22. In an effort to expedite favorable prosecution, Applicants have cancelled claim 27, without prejudice.

Regarding claims 28 and 35, the Examiner is unclear as to the meaning of “non-compact” configurations. In this regard, Applicants direct the Examiner’s attention to the specification at page 8, lines 20-31 wherein “non-compact” configurations are defined and eliminated consistent with the method of Flower, *J. Molecular Graphics and Modeling* 1997 15(4):238-244.

Claims 29, 36 and 38 are similarly rejected as allegedly indefinite. Applicants respectfully direct the Examiner’s attention to the specification, at page 10, line 19-page 11, line 7 wherein the similarity of patterns of surface exposure are defined in terms of clustered configurations of protein sequences. A detailed method for clustering is also described therein.

Finally, claims 30 and 34 are rejected as allegedly indefinite. Applicants respectfully submit that the “each configuration” recitation refers to the clustered configurations of the preceding claims. Moreover, the recitation “designing proteins” in the fourth line of the

claim (which Applicants believe that Examiner objects to) refers to the selection of proteins having the highest Variance.

Thus, in view of the foregoing remarks, the rejection of claims 22-40 under 35 U.S.C. §112, second paragraph is overcome and withdrawal thereof is respectfully requested.

Claims 22-40 have been rejected under 35 U.S.C. §112, first paragraph, as allegedly lacking enabling support. Applicants respectfully submit that the pending claims are fully supported by the disclosure of the specification which embodies a method, which is useful for identifying protein backbone configurations, generated from specified phi-psi angle pairs. The method of the present invention is fully supported by the disclosure. The Examiner's attention is respectfully directed to page 6, lines 28-page 13, line 19 of the specification. Accordingly, the rejection of claims 22-40 under 35 U.S.C. §112, first paragraph is overcome and withdrawal thereof is respectfully requested.

Claims 22-40 have also been rejected under 35 U.S.C. §§101/112, first paragraph as allegedly lacking a substantially utility or well-established utility. Applicants respectfully submit that the pending claims, serve to clarify the utility of the claimed invention which is in the context of a method for identifying protein backbone configurations. Applicants submit that it is the claimed invention that is the focus of the utility requirement. See MPEP §2107.02. Inasmuch as the Applicants have clearly established utility for a method for identifying protein backbone configurations, any rejection under 35 U.S.C. §§101/112, first paragraph is improper and should be withdrawn.

Thus, the present application is condition for allowance, which action is earnestly solicited.

Respectfully submitted,

A handwritten signature in black ink, appearing to read "Peter I. Bernstein", with a stylized flourish at the end.

Peter I. Bernstein

Registration No. 43,497

Scully, Scott, Murphy & Presser
400 Garden City Plaza
Garden City, New York 11530
(516) 742-4343

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